A photograph of a busy city street at night, filled with cars and streetlights. The scene is illuminated by warm yellow streetlights and the headlights of the vehicles. In the background, there are buildings and a large digital billboard. The overall atmosphere is one of a bustling urban environment.

IdentiPROT

**комплексное решение для потока протеемных данных
по принципу «все включено»**

The image shows a browser window with several tabs open. The active tab is titled "Welcome to Ide...". The address bar shows the URL "identiprot.theorchromo.ru/logout/". The page content includes a large blue header with the text "IdentiPROT" and navigation links for "ABOUT", "LOG IN", and "CONTACTS". Below the header, there is a main heading "Welcome to the home of IdentiPROT software!" followed by a paragraph: "If you have problems logging in, any questions or comments, please [contact](#) our administrators to create account." To the right, there is a dark blue box with the text "WELCOME The single entry point for your proteomic data mining". Below this box are two input fields labeled "Email" and "Password", and a large blue "Log in" button.

Вход через Интернет из клиентского места, включая мобильные устройства

New Search

identiprot.theorchromo.ru/data/

load parameters

send email notification

use auto optimization

enzyme: [add custom cleavage rule](#) trypsin

number of missed cleavages 2

precursor accuracy unit ppm

precursor accuracy left 10

precursor accuracy right 10

precursor isotope mass error 0

product accuracy, Da 0.1

FDR 1.0

FDR type psm

minimum charge 2

maximum charge 3

generate decoy db no

decoy method reverse

decoy prefix DECOY_

dynamic range 100

peptide minimum length 5



Ввод параметров поиска

New Search

identiprot.theorchromo.ru/data/

matched fragments, min 1

use scoring function hypscore

score threshold 0

show unmatched spectra in results no

report number of sequence candidates 1

[select fixed modifications](#) camC

[select potential modifications](#)

peptide mass shift 0

Post-search validation

PSM count

PSMs per protein

charge states

potential modifications

fragment mass tolerance

precursor mass difference

isotopes mass error

missed cleavages

RT difference

Enter search run name

RUNIDENTIPROT

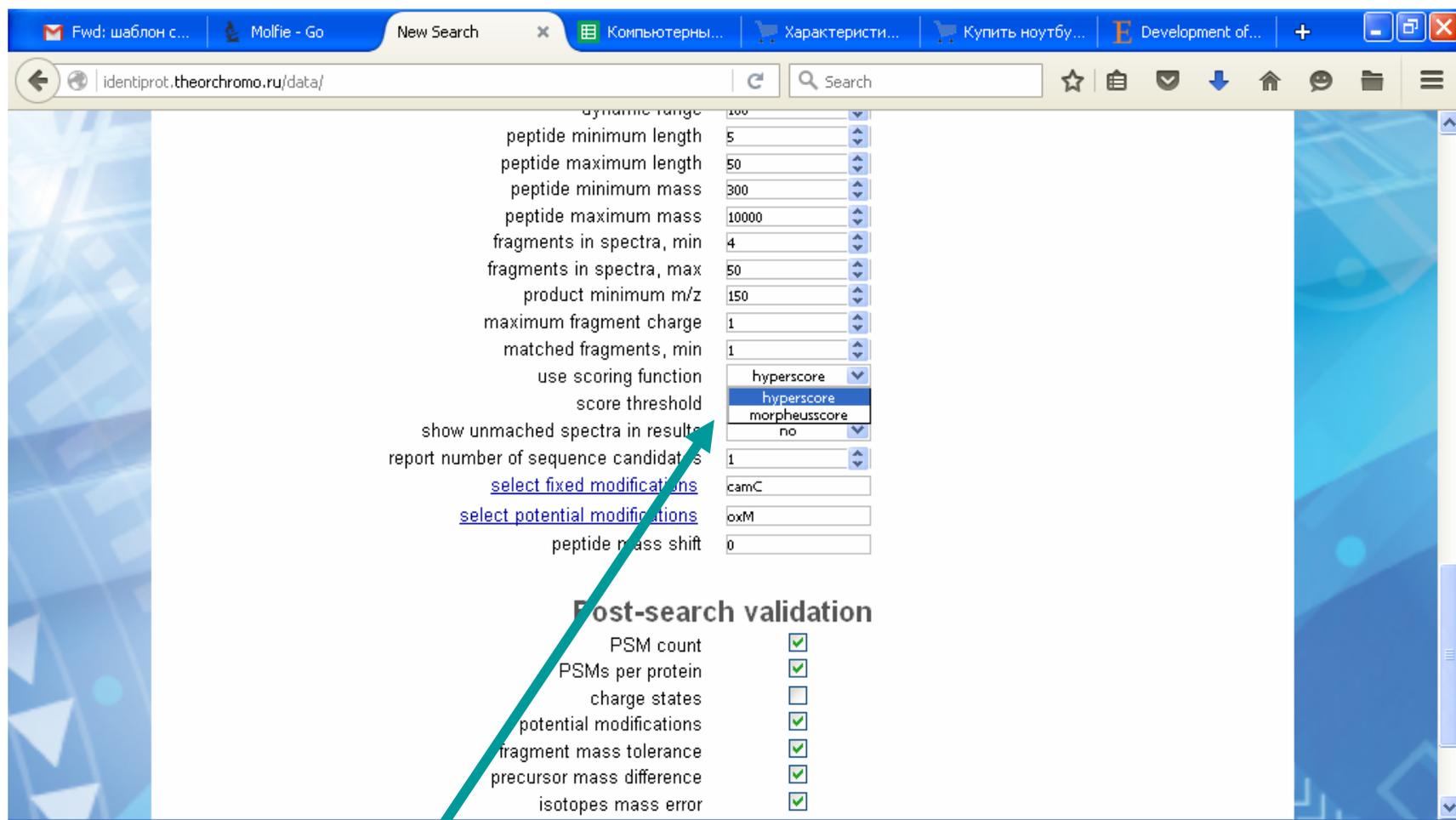
Clear chosen files



Послепоисковое
валидирование
идентификаций
(до 9 ортогональных
критериев)

The screenshot shows the IDENTIPROT web interface. At the top, there is a navigation bar with several tabs: "Fwd: шаблон с...", "Molfie - Go", "New Search", "Компьютерны...", "Характеристи...", "Купить ноутбу...", and "Development of...". Below the navigation bar is a search bar with the URL "identiprot.theorchromo.ru/data/" and a search button. The main content area is titled "Choose preloaded protein database file" and includes a text input field for "Enter search run name" and a large yellow button labeled "RUN IDENTIPROT". Below this is a section titled "Specify search parameters" with three tabs: "MINIMAL", "MEDIUM", and "ADVANCED". The "ADVANCED" tab is selected, showing various search parameters with input fields and dropdown menus. A green arrow points to the "use auto optimization" checkbox, which is checked. The parameters listed are: "send email notification" (checkbox), "use auto optimization" (checkbox), "enzyme: [add custom cleavage rule](#)" (dropdown menu with "trypsin" selected), "number of missed cleavages" (input field with "5"), "precursor accuracy unit" (dropdown menu with "ppm"), "precursor accuracy left" (input field with "10"), "precursor accuracy right" (input field with "10"), "precursor isotopic mass error" (input field with "0"), "product accuracy, Da" (input field with "0.05"), "FDR" (input field with "1"), "FDR type" (dropdown menu with "protein"), "minimum charge" (input field with "2"), and "maximum charge" (input field with "5").

Автоматическая оптимизация входных параметров поиска под конкретные данные



Выбор сторонней скоринг-функции в режиме выбора параметров поиска «Advanced»

The image displays two screenshots of the IdentiPROT web application. The top screenshot shows the main interface with a search history table. A teal arrow points from the 'testsearch01' entry to the bottom screenshot. The bottom screenshot shows the search results page for 'testsearch01/test', including a summary table, download options, and three histograms showing PSM distributions for retention time, precursor m/z, and peptide length.

Вывод результатов поиска

START A NEWSEARCH RUN

Интерактивный просмотр идентификаций и их распределений по экспериментальным параметрам и физико-химическим свойствам пептидов

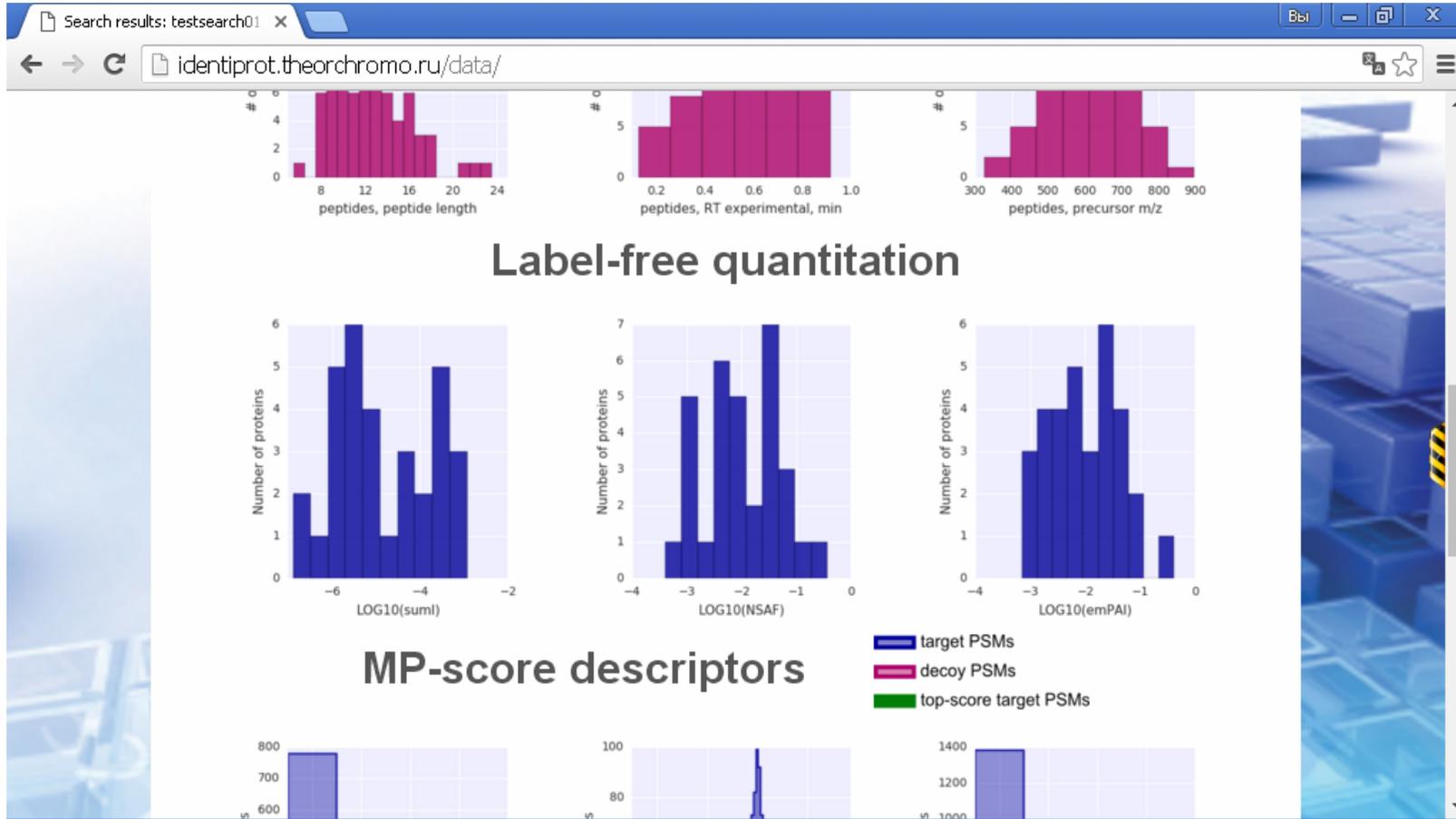
Search name	PSMs	Peptides	Proteins	FDR, %	FDR type	MS/MS	Unfiltered PSMs
test	178	82	32	1.0	psm	3000	2356

Download: [csv files](#) [pepxml files](#) [mgf files](#)
[figures in png format](#) [figures in svg format](#) [show parameters](#)

PSM distributions

Three histograms showing the distribution of PSMs across different parameters:

- PSMs RT experimental_min: Distribution of retention times, peaking around 0.7-0.8 minutes.
- PSMs precursor m/z: Distribution of precursor mass-to-charge ratios, peaking around 450-500 m/z.
- PSMs peptide length: Distribution of peptide lengths, peaking around 10-12 amino acids.



Расчет трех количественных индексов относительного содержания идентифицированных белков

The image shows two browser windows. The top window displays search results from identiprot.theorchromo.ru for the search name '2016-08-10 19-02-45/ 20160809 01 HeLa'. A table lists search results with columns for Search name, PSMs, Peptides, Proteins, FDR, FDR type, MS/MS, and Unfiltered PSMs. Below the table is a 'Select columns for proteins:' section with checkboxes for various data fields. A table below this section lists protein dbnames and their corresponding PSM counts.

Search name	PSMs	Peptides	Proteins	FDR, %	FDR type	MS/MS	Unfiltered PSMs
20160809_01_HeLa	20521	18718	3870	1.0			

Select columns for proteins:

dbname description PSMs peptides sequence coverage
 LFQ(S/n) LFQ(NSAF) LFQ(emPAI) protein LN(e value) all proteins

dbname	PSMs
sp P38646 GRP75_HUMAN	38
sp Q9UKI8-3 ITLK1_HUMAN	1
sp O75694-2 INU155_HUMAN	10
sp P50995 JANX11_HUMAN	8
sp P15880 IRS2_HUMAN	17
sp P07108-4 JACBP_HUMAN	2
sp Q9HC68 CWC22_HUMAN	1

The bottom window shows the UniProtKB entry for P38646 (GRP75_HUMAN). The entry title is 'UniProtKB - P38646 (GRP75_HUMAN)'. The protein is identified as 'Stress-70 protein, mitochondrial' and is from the organism 'Homo sapiens (Human)'. The gene is 'HSPA9'. The entry includes options for BLAST, Align, Format, Add to basket, and History.

Интерактивный режим просмотра белковых identifications

Fwd: шаблон с... Molfie - Go Contacts x Компьютерны... Характеристики... Купить ноутбу... Development of... +

identiprot.theorchromo.ru/data/ Search

IDENTIPROT START SEARCH UPLOAD FILES SEARCH HISTORY CONTACTS

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Наши специалисты всегда с вами!